RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10689,677 B

Source: PFWO

Date Processed by STIC: 5/14/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE).
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450.
3. Hand Carry directly to (EFFECTIVE 12/01/03):
    U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10 689,677 B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
Wrapped Aminos — The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 _____ Invalid Line Length — The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 _____ Misaligned Amino
Numbering — The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 _____ Non-ASCII — The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 _____ Variable Length — Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 _____ PatentIn 2.0
"bug" — A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 _____ Skipped Sequences
(OLD RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 _____ Skipped Sequences
(NEW RULES) — Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 _____ Use of n's or Xaa's
(NEW RULES) — Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 _____ Invalid <213>
Response — Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

11 _____ Use of <220> — Sequence(s) *3-6* missing the <220> "Feature"
✱Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12 _____ PatentIn 2.0
"bug" — Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 _____ Misuse of n/Xaa — "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC – Biotechnology Systems Branch – 09/09/2003

IFWO

RAW SEQUENCE LISTING   DATE: 05/14/2004
PATENT APPLICATION: US/10/689,677B   TIME: 16:08:12

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\05142004\J689677B.raw**

```
   5 <110> APPLICANT: Wyeth
   6        Wolfman, Neil
   7        Bouxsein, Mary
   9 <120> TITLE OF INVENTION: ActRIIB Fusion polypeptides and Uses Therefor
  11 <130> FILE REFERENCE: 08702.6093-00000
W--> 12 <140> CURRENT APPLICATION NUMBER: 10/689,677B
C--> 13 <141> CURRENT FILING DATE: 2003-10-22
  13 <150> PRIOR APPLICATION NUMBER: October 22, 2003
W--> 14 <160> NUMBER OF SEQ ID: 6
  16 <170> SOFTWARE: PatentIn version 3.1
```

ERRORED SEQUENCES

```
 199 <210> SEQ ID NO: 3
 200 <211> LENGTH: 378
 201 <212> TYPE: PRT
 202 <213> ORGANISM: Artificial Sequence
W--> 203 <220> FEATURE:
 203 <223> OTHER INFORMATION: Chimera/Fusion
  --> 205 <400> SEQUENCE: 3
 207 Met Lys Phe Leu Val Asn Val Ala Leu Val Phe Met Val Val Tyr Ile
 208 1               5                  10                  15
 210 Ser Tyr Ile Tyr Ala Thr Ser Gly Arg Gly Glu Ala Glu Thr Arg Glu
 211             20                  25                  30
 213 Cys Ile Tyr Tyr Asn Ala Asn Trp Glu Leu Glu Arg Thr Asn Gln Ser
 214             35                  40                  45
 216 Gly Leu Glu Arg Cys Glu Gly Glu Gln Asp Lys Arg Leu His Cys Tyr
 217     50                  55                  60
 219 Ala Ser Trp Arg Asn Ser Ser Gly Thr Ile Glu Leu Val Lys Lys Gly
 220 65                  70                  75                  80
 222 Cys Trp Leu Asp Asp Phe Asn Cys Tyr Asp Arg Gln Glu Cys Val Ala
 223             85                  90                  95
 225 Thr Glu Glu Asn Pro Gln Val Tyr Phe Cys Cys Cys Glu Gly Asn Phe
 226             100                 105                 110
 228 Cys Asn Glu Arg Phe Thr His Leu Pro Glu Ala Gly Gly Pro Glu Val
 229         115                 120                 125
 230 Thr Tyr Glu Pro Pro Pro Thr Ala Pro Thr Gly Gly Arg Gly Asp Asp
 231     130                 135                 140
 233 Asp Asp Lys Thr Arg Ser Arg Asp Lys Thr His Thr Cys Pro Pro Cys
 234 145                 150                 155                 160
 236 Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro
 237             165                 170                 175
```

Handwritten annotations:
- Does Not Comply Corrected Diskette Needed (pg. 1-4)
- <220> FEATURE: — pls insert this mandatory, numeric identifier, with NO response.
- please see item #11 on error summary sheet.

```
239 Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys
240             180             185             190
242 Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp
243         195             200             205
245 Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu
246     210             215             220
248 Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu
249 225             230             235             240
251 His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn
252             245             250             255
254 Lys Ala Leu Pro Val Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly
255             260             265             270
257 Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu
258         275             280             285
260 Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr
261     290             295             300
263 Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn
264 305             310             315             320
266 Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe
267             325             330             335
269 Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn
270             340             345             350
272 Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr
273         355             360             365
275 Gln Lys Ser Leu Ser Leu Ser Pro Pro Lys
276     370             375
278 <210> SEQ ID NO: 4
279 <211> LENGTH: 1134
280 <212> TYPE: DNA
281 <213> ORGANISM: Artificial Sequence
282 <220> FEATURE:
282 <223> OTHER INFORMATION: Chimera/Fusion
284 <400> SEQUENCE: 4
285 atgaaattct tagtcaacgt tgcccttgtt tttatggtcg tgtacatttc ttacatctat     60
287 gcgactagtg ggcgtgggga ggctgagaca cgggagtgca tctactacaa cgccaactgg    120
288 gagctggagc gcaccaacca gagcggcctg gagcgctgcg aaggcgagca ggacaagcgg    180
290 ctgcactgct acgcctcctg gcgcaacagc tctggcacca tcgagctcgt gaagaagggc    240
292 tgctggctag atgacttcaa ctgctacgat aggcaggagt gtgtggccac tgaggagaac    300
294 ccccaggtgt acttctgctg ctgtgaaggc aacttctgca cgagcgctt cactcatttg    360
296 ccagaggctg ggggcccgga agtcacgtac gagccacccc cgacagcccc caccggcggc    420
298 cgcggagacg acgacgacaa gacgcgttct agagacaaaa ctcacacatg cccaccgtgc    480
300 ccagcacctg aactcctggg gggaccgtca gtcttcctct tccccccaaa acccaaggac    540
302 accctcatga tctcccggac ccctgaggtc acatgcgtgg tggtggacgt gagccacgaa    600
304 gaccctgagg tcaagttcaa ctggtacgtg gacggcgtgg aggtgcataa tgccaagaca    660
306 aagccgcggg aggagcagta caacagcacg taccgtgtgg tcagcgtcct caccgtcctg    720
308 caccaggact ggctgaatgg caaggagtac aagtgcaagg tctccaacaa agccctccca    780
310 gtccccatcg agaaaaccat ctccaaagcc aaaggcagc cccgagaacc acaggtgtac    840
312 accctgcccc catcccggga ggagatgacc aagaaccagg tcagcctgac ctgcctggtc    900
314 aaaggcttct atcccagcga catcgccgtg gagtgggaga gcaatgggca gccggagaac    960
```

RAW SEQUENCE LISTING DATE: 05/14/2004
PATENT APPLICATION: US/10/689,677B TIME: 16:08:12

Input Set : A:\PTO.FG.txt
Output Set: N:\CRF4\05142004\J689677B.raw

```
316 aactacaaga ccacgcctcc cgtgctggac tccgacggct ccttcttcct ctatagcaag   1020
318 ctcaccgtgg acaagagcag gtggcagcag gggaacgtct tctcatgctc cgtgatgcat   1080
320 gaggctctgc acaaccacta cacgcagaag agcctctccc tgtccccgcc taaa          1134
322 <210> SEQ ID NO: 5
323 <211> LENGTH: 4
324 <212> TYPE: PRT
325 <213> ORGANISM: Artificial Sequence
```
W--> 326 <220> FEATURE: ~ pls insert
```
326 <223> OTHER INFORMATION: Linking Sequence, Gly-Ser repeat
```
E--> 328 <400> SEQUENCE: 5
```
330 Gly Ser Gly Ser
331 1
333 <210> SEQ ID NO: 6
334 <211> LENGTH: 4
335 <212> TYPE: PRT
336 <213> ORGANISM: Artificial Sequence
```
W--> 337 <220> FEATURE: ~ pls insert
```
337 <223> OTHER INFORMATION: Linking Sequence, Enterokinase Cleavage Site
```
E--> 339 <400> SEQUENCE: 6
```
341 Asp Asp Asp Lys
342 1
```

VERIFICATION SUMMARY   DATE: 05/14/2004
PATENT APPLICATION: **US/10/689,677B**   TIME: 16:08:13

Input Set : **A:\PTO.FG.txt**
Output Set: **N:\CRF4\05142004\J689677B.raw**

L:12 M:283 W: Missing Blank Line separator, <140> field identifier
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:14 M:283 W: Missing Blank Line separator, <160> field identifier
L:203 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:205 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:3
L:282 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:284 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:4
L:326 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:5
L:328 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:5
L:337 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:339 M:200 E: Mandatory Header Field missing, <220> Tag not found for SEQ ID#:6